

**FUNCTIONAL CHARACTERIZATION OF *Pseudomonas aeruginosa*  
VIRULENCE-RELATED GENES LOCATED IN A PATHOGENICITY ISLAND.**

Gianlucca Gonçalves Nicastro and Regina L. Baldini  
Departamento de Bioquímica, IQ, USP, São Paulo, Brazil

*Pseudomonas aeruginosa* (*Pa*) is a gammaproteobacterium that behaves as an opportunistic pathogen to a broad range of hosts. Strain PA14 carries the pathogenicity island PAPI-1 that contains several virulence-related genes of unknown function. Between two copies of direct repeat sequences in PAPI-1, there are two pairs of two-component regulatory systems, *pvrSR* and *rscCB* and a putative fimbrial chaperone-usher gene cluster named *cupD*. In an attempt to uncover the functions of *pvrSR* and *rscCB*, the phenotypes of non-polar mutant strains in each of the four genes were analyzed. No consistent differences were seen regarding swimming, swarming and twitching motilities of the mutant strains as compared to the wild-type. The strain with a deletion in *pvrR*, which codes for a response regulator containing an EAL domain, was slightly impaired in biofilm formation. Furthermore, strains lacking the histidine kinase RcsC and the predicted transcriptional activator RcsB presented variations in the length of the lipopolysaccharide O-antigen chains, suggesting that this pair of genes function together. Whether the expression of the *wzz* genes, which controls the length of O-antigen chain, is altered in the *rscC* and *rscB* mutant strains is currently under investigation. If this hypothesis is confirmed, this will be the first example of gene(s) in the core genome of *Pa* shown to be under regulation of genes located in a genomic island.

Acknowledgements: CNPq and FAPESP

Key-words: *Pseudomonas aeruginosa*, pathogenicity island, two-component systems